



EI124979222US

ABX-INR/004 CIP

Examiner : Not yet assigned
Group Art Unit : 1646
Applicants : James S. Huston et al.
Application No. : 09/620,955 Confirmation No. 4028
Filed : July 21, 2000
For : METHODS AND COMPOSITIONS FOR INHIBITING
POLYPEPTIDE ACCUMULATION ASSOCIATED WITH
NEUROLOGICAL DISORDERS

Hon. Commissioner
for Patents
Washington, D.C. 20231

New York, New York
January 30, 2002

TRANSMITTAL LETTER

Sir:

Transmitted herewith: ☒ a Preliminary Amendment;
☒ a Response to Notice to Comply With Sequence Listing
Rules; ☒ copy of Notice to Comply With Sequence Listing
Rules; ☒ substitute Sequence Listing pages 1-18; ☒
substitute diskette; ☒ Statement Under 37 C.F.R. §§ 1.825(a)
and (b); to be filed in the above-identified patent
application.

FEE FOR ADDITIONAL CLAIMS

☒ A fee for additional claims is not required.

☐ A fee for additional claims is required.

The additional fee has been calculated as shown below:

CLAIMS REMAINING AFTER AMENDMENT	HIGHEST NUMBER PREVIOUSLY PAID FOR	PRESENT EXTRA	RATE	ADDITIONAL FEES
TOTAL CLAIMS	-	* =	X \$ 18 =	\$
INDEPENDENT CLAIMS	-	** =	X \$ 84 =	\$
FIRST PRESENTATION OF A MULTIPLE DEPENDENT CLAIM			+ \$280 =	\$
* If less than 20, insert 20.			TOTAL	\$

** If less than 3, insert 3.

[] A check in the amount of \$_____ in payment of the filing fee is transmitted herewith.

[X] The Director is hereby authorized to charge payment of any additional filing fees required under 37 C.F.R. § 1.16, in connection with the paper(s) transmitted herewith, or credit any overpayment of same, to deposit Account No. 06-1075. A duplicate copy of this transmittal letter is transmitted herewith.

[] Please charge \$_____ to Deposit Account No. 06-1075 in payment of the filing fee. A duplicate copy of this transmittal letter is transmitted herewith.

EXTENSION FEE

[] The following extension is applicable to the Response filed herewith; [] \$110.00 extension fee for response within first month pursuant to 37 C.F.R. § 1.136(a); [] \$400.00 extension fee for response within second month pursuant to 37 C.F.R. § 1.136(a); [] \$920.00 extension fee for response within third month pursuant to 37 C.F.R. § 1.136(a); [] \$1,440.00 extension fee for response within fourth month pursuant to 37 C.F.R.

§ 1.136(a); \$1,960.00 within fifth month pursuant to
37 C.F.R. § 1.136(a).

☐ A check in the amount of ☐ \$110.00; ☐ \$400.00;
☐ \$920.00; ☐ \$1,440.00; ☐ \$1,960.00 in payment
of the extension fee is transmitted herewith.

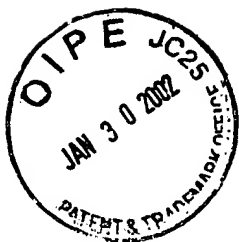
☒ The Director is hereby authorized to charge payment
of any additional fees required under 37 C.F.R. §
1.17 in connection with the paper(s) transmitted
herewith, or to credit any overpayment of same, to
Deposit Account No. 06-1075. A duplicate copy of
this transmittal letter is transmitted herewith.

☐ Please charge the ☐ \$110.00; ☐ \$400.00;
☐ \$920.00; ☐ \$1,440.00; ☐ \$1,960.00; extension
fee to Deposit Account No. 06-1075. A duplicate
copy of this transmittal letter is transmitted
herewith.



Jane T. Gunnison (Reg. No. 38,479)
Attorney for Applicants
Haitao Sun (Reg. No. 48,546)
Agent for Applicants

FISH & NEAVE
1251 Avenue of the Americas
New York, New York 10020-1105
Tel.: (212) 596-9000



PATENTS

ABX-INR/004 CIP

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT APPLICATION

Examiner : Not yet assigned
Group Art Unit : 1646
Applicants : James S. Huston et al.
Application No. : 09/620,955 Confirmation No. 4028
Filed : July 21, 2000
For : METHODS AND COMPOSITIONS FOR
INHIBITING POLYPEPTIDE ACCUMULATION
ASSOCIATED WITH NEUROLOGICAL
DISORDERS

EXPRESS MAIL CERTIFICATION

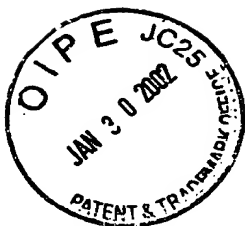
"Express Mail" mailing label number EI124979222US

Date of Deposit January 30, 2002.

I hereby certify that this transmittal letter and the other papers and fees identified in this transmittal letter as being transmitted herewith are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. * 1.10 on the date indicated above and are addressed to the Hon. Commissioner for Patents, P.O. Box 2327 Arlington VA 22202.


Lillian Garcia

1. Transmittal Letter (in duplicate)
2. Preliminary Amendment
3. Response to Notice to Comply with Sequence Listing Rules
4. Copy of Notice to Comply with Sequence Listing Rules
5. Substitute Sequence Listing pages 1-18
6. Substitute diskette
7. Statement under 37 C.F.R. §§ 1.825 (a) and (b)

ABX-INR/004 CIP

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Examiner : Not yet assigned
Group Art Unit : 1646
Applicants : James S. Huston et al.
Application No. : 09/620,955 Confirmation No.: 4028
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For : METHODS AND COMPOSITIONS FOR INHIBITING
POLYPEPTIDE ACCUMULATION ASSOCIATED WITH
NEUROLOGICAL DISORDERS

New York, New York
January 30, 2002

Hon. Commissioner for Patents
Washington, D.C. 20231

RESPONSE TO NOTICE TO COMPLY

Sir:

This is in response to a November 30, 2001 Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures ("the Notice", a copy of which is attached). The Notice states that the Sequence Listing, as filed, contains errors relating to the use of Xaa in SEQ ID NOS: 9, 10 and 12-20. Specifically, applicants were required to submit a substitute Sequence Listing indicating the location of the Xaa in each sequence.

Applicants have instead deleted the symbol Xaa from SEQ ID NOS: 9, 10, 12, 13, 14, 15, 16, 17, 18, 19 and 20, and have replaced the symbol with the actual residue symbols indicated in

<220> to <223> section of the original Sequence Listing as shown in the following table.

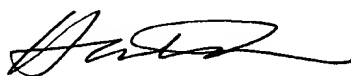
<u>SEQ ID NO:</u>	<u>Former sequence: Xaa at position</u>	<u>Replaced in amendment by</u>
9	15	35 Gln's
10	24	25 Gln's
12	18	47 Gln's
13	18	72 Gln's
14	18	104 Gln's
15	18	47 Gln's
16	18	72 Gln's
17	18	104 Gln's
18	34	25 Gln's
19	34	104 Gln's
20	25	81 Gln's

None of the above amendments adds new matter.

Further, applicants noted that SEQ ID NO: 11 inadvertently omitted the Xaa, which should have been positioned between residue Phe at position 23 and residue Leu at position 24 in the original Sequence Listing. However, the specification at page 43, Table 3 indicates the location of the Xaa in SEQ ID NO: 11. Both said Table 3 and fields <220> to <223> of SEQ ID NO: 11 in the original Sequence Listing indicate that Xaa stands for 42 Gln residues. Accordingly, applicants have inserted 42 Gln's into SEQ ID NO: 11 at the above-indicated position.

We enclose herewith a diskette containing a computer readable form of the amended Sequence Listing, a paper copy of the Sequence Listing (pages 1-18) and a statement that the content of the paper Sequence Listing and the diskette Sequence Listing are the same and do not include new matter.

Respectfully submitted,



Jane T. Gunnison (Reg. No. 38,479)
Attorney for Applicants
Haitao Sun (Reg. No. 48,546)
Agent for Applicants
c/o FISH & NEAVE
1251 Avenue of the Americas
New York, New York 10020
Tel.: (212) 596-9000
Fax.: (212) 596-9090

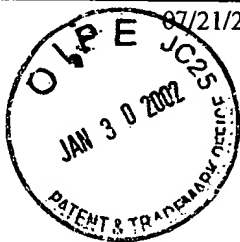


UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/620,955	07/21/2000	James S. Huston	INR-004CP

000959
LAHIVE & COCKFIELD
28 STATE STREET
BOSTON, MA 02109



CONFIRMATION NO. 4028

FORMALITIES LETTER



OC000000007144104

Date Mailed: 11/30/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

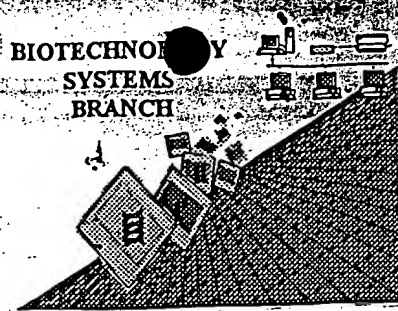
- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

*A copy of this notice **MUST** be returned with the reply.*

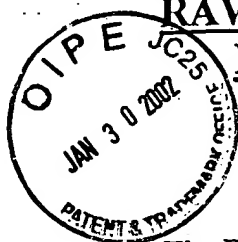
Customer Service Center

Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE



2570
1113



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/620,955A

Source: OIPE

Date Processed by STIC: 11/16/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

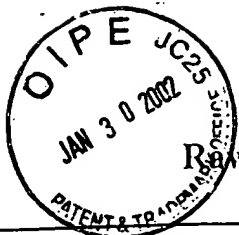
Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

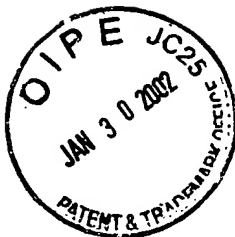
ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 091620,955A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/620,955A

DATE: 11/16/2001
TIME: 10:27:12

Input Set : A:\seqlist.txt

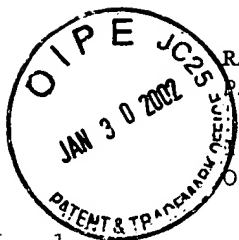
Output Set: N:\CRF3\11162001\I620955A.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: Huston, James s
4 Messer, Anne
5 Lecerf, Jean-Michel
7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
8 ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
10 <130> FILE REFERENCE: INR-004CP
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/620,955A
C--> 13 <141> CURRENT FILING DATE: 2000-07-21
15 <150> PRIOR APPLICATION NUMBER: 60/146,047
16 <151> PRIOR FILING DATE: 1999-07-27
18 <160> NUMBER OF SEQ ID NOS: 45
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 345
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
29 construct
31 <220> FEATURE:
32 <223> OTHER INFORMATION: The VH sequence uses a V segment of the VH3
33 family.
35 <220> FEATURE:
36 <223> OTHER INFORMATION: CDR1 sequence: from base 91 to base 105 (15
37 bases).
39 <220> FEATURE:
40 <223> OTHER INFORMATION: CDR2 sequence: from base 148 to base 198 (51
41 bases).
43 <220> FEATURE:
44 <223> OTHER INFORMATION: CDR3 sequence: from base 295 to base 312 (18
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48 caggtgcagc tgcaggagtc ggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
49 tctgtgagc cctctggatt caccctcagt agttatagca tgagctgggt ccgccaggct 120
50 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180
51 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cagctgtat 240
52 cttcaaataga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatagg 300
53 tacttcgatc tctggggccg tggcaccctg gtcaccgtct cctca 345
55 <210> SEQ ID NO: 2
56 <211> LENGTH: 115
57 <212> TYPE: PRT
58 <213> ORGANISM: Artificial Sequence
60 <220> FEATURE:
61 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
62 construct
64 <400> SEQUENCE: 2
65 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

Errors on pp. 5

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/620,955A

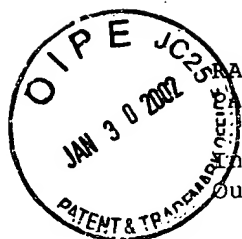
DATE: 11/16/2001

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

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66      1      5      10      15
68 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
69      20      25      30
71 Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
72      35      40      45
74 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
75      50      55      60
77 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
78 65      70      75      80
80 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
81      85      90      95
83 Ala Arg Asp Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
84      100      105      110
86 Val Ser Ser
87      115
90 <210> SEQ ID NO: 3
91 <211> LENGTH: 327
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
97      construct
99 <220> FEATURE:
100 <223> OTHER INFORMATION: The VL sequence uses a V segment of the VL2
101      family.
103 <220> FEATURE:
104 <223> OTHER INFORMATION: CDR1 sequence: from base 67 to base 108 (42
105      bases).
107 <220> FEATURE:
108 <223> OTHER INFORMATION: CDR2 sequence: from base 154 to base 174 (21
109      bases).
111 <220> FEATURE:
112 <223> OTHER INFORMATION: CDR3 sequence: from base 271 to base 294 (24
113      bases).
115 <400> SEQUENCE: 3
116 cagtctgcc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
117 tcttgcactg gaaccagcag tgacattggt gcttataact atgtctcctg gtaccagcag 120
118 tatccaggca aggccccaa actccttatt tatgatgtca gtaatcggcc ctcagggatt 180
119 tctaategct tctctggctc caagtctggc gatacggcct ccctgaccat ctctgggctc 240
120 caggctgagg acgaggctga ttattactgc agctcatttg cgaacagcgg ccccttattc 300
121 ggcggaggga ccaaggtcac cgtccta 327
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 109
125 <212> TYPE: PRT
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
130      construct
132 <400> SEQUENCE: 4
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/620,955A

DATE: 11/16/2001

TIME: 10:27:12

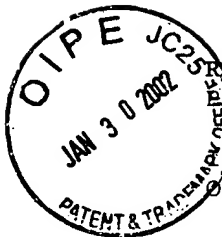
Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

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134   1           5           10           15
136 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly Ala Tyr
137           20           25           30
139 Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro Lys Leu
140           35           40           45
142 Leu Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Ile Ser Asn Arg Phe
143           50           55           60
145 Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser Gly Leu
146   65           70           75           80
148 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala Asn Ser
149           85           90           95
151 Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
152           100          105
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 717
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
162   construct
164 <400> SEQUENCE: 5
165 cagggtgcagc tgcaggagtc ggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
166 tctgtgtcag cctctggatt caccctcagt agttatagca tgagctgggt ccgccaggct 120
167 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180
168 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cagctgtat 240
169 cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatagg 300
170 tacttcgata tctggggccg tggcaccctg gtcaccgtct cctcagggtg aggcgggtca 360
171 ggcgagggtg gctctggcgg tggcgatcgc cagtctgccc tgactcagcc tgcctccgtg 420
172 tctgggtctc ctggacagtc gatcaccatc tctgcaactg gaaccagcag tgacattggt 480
173 gcttataact atgtctcctg gtaccagcag tatccaggca aggcctccaa actccttatt 540
174 tatgatgtca gtaatcggcc ctccaggatt tctaactcgt tctctggctc caagtctggc 600
175 gatacggcct cctgaccat ctctgggctc caggctgagg acgaggctga ttattactgc 660
176 agctcatttg cgaacagcgg ccccttattc ggcggaggga ccaaggtcac cgtccta 717
178 <210> SEQ ID NO: 6
179 <211> LENGTH: 239
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
185   construct
187 <400> SEQUENCE: 6
188 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
189   1           5           10           15
191 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
192           20           25           30
194 Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
195           35           40           45
197 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

```



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/620,955A

DATE: 11/16/2001

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

198 50 55 60
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
201 65 70 75 80
203 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
204 85 90 95
206 Ala Arg Asp Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
207 100 105 110
209 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
210 115 120 125
212 Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro
213 130 135 140
215 Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly
216 145 150 155 160
218 Ala Tyr Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro
219 165 170 175
221 Lys Leu Leu Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Ile Ser Asn
222 180 185 190
224 Arg Phe Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser
225 195 200 205
227 Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala
228 210 215 220
230 Asn Ser Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
231 225 230 235

234 <210> SEQ ID NO: 7

235 <211> LENGTH: 44

236 <212> TYPE: DNA

237 <213> ORGANISM: Artificial Sequence

239 <220> FEATURE:

240 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

241 construct

243 <400> SEQUENCE: 7

244 tcaccgtctc ctcaggtgga ggcggttcag gcggaggtgg ctct

44

246 <210> SEQ ID NO: 8

247 <211> LENGTH: 48

248 <212> TYPE: DNA

249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

252 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

253 construct

255 <400> SEQUENCE: 8

256 tgggtgagct catgtccgmt ccgccaccgc cagagccacc tccgcctg

48

258 <210> SEQ ID NO: 9

259 <211> LENGTH: 35

260 <212> TYPE: PRT

261 <213> ORGANISM: Artificial Sequence

263 <220> FEATURE:

264 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

265 construct

267 <220> FEATURE:

RAW SEQUENCE LISTING

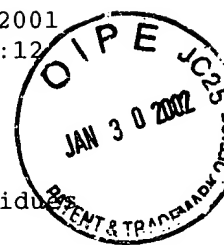
DATE: 11/16/2001

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*Must give location
of Xaa, see error
summary sheet,
item 9*

268 <223> OTHER INFORMATION: where X represents 35 glutamine (Q) residues
 270 <400> SEQUENCE: 9
 W--> 271 Leu Val Pro Arg Gly Ser Val Ser Thr His His His His His Xaa His
 272 1 5 10 15
 274 His Gly Asn Ser Gly Pro Pro Glu Phe Pro Gly Arg Leu Glu Arg Pro
 275 20 25 30
 277 His Arg Asp
 278 35
 281 <210> SEQ ID NO: 10
 282 <211> LENGTH: 35
 283 <212> TYPE: PRT
 284 <213> ORGANISM: Artificial Sequence
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 288 construct
 290 <220> FEATURE: *same error*
 291 <223> OTHER INFORMATION: where X represents 25 glutamine (Q) residues
 293 <400> SEQUENCE: 10
 294 Leu Val Pro Arg Gly Ser Met Ala Thr Leu Glu Lys Leu Met Lys Ala
 295 1 5 10 15
 W--> 297 Phe Glu Ser Leu Lys Ser Phe Xaa Leu Gln Pro Gly Ser Thr Arg Ala
 298 20 25 30
 300 Ala Ala Ser
 301 35
 304 <210> SEQ ID NO: 11
 305 <211> LENGTH: 34
 306 <212> TYPE: PRT
 307 <213> ORGANISM: Artificial Sequence
 309 <220> FEATURE:
 310 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 311 construct
 313 <220> FEATURE:
 314 <223> OTHER INFORMATION: where X represents 42 glutamine (Q) residues
 316 <400> SEQUENCE: 11
 317 Leu Val Pro Arg Gly Ser Met Ala Thr Leu Glu Lys Leu Met Lys Ala
 318 1 5 10 15
 320 Phe Glu Ser Leu Lys Ser Phe Leu Gln Pro Gly Ser Thr Arg Ala Ala
 321 20 25 30
 323 Ala Ser
 327 <210> SEQ ID NO: 12
 328 <211> LENGTH: 18
 329 <212> TYPE: PRT
 330 <213> ORGANISM: Artificial Sequence
 332 <220> FEATURE:
 333 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 334 construct
 336 <220> FEATURE:
 337 <223> OTHER INFORMATION: where X represents 47 glutamine (Q) residues
 339 <400> SEQUENCE: 12



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/620,955A

DATE: 11/16/2001

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:271 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:271 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:383 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:383 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:429 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:429 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:484 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:484 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:507 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:507 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:527 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:527 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20